



#6

SEQUENCE LISTING

<110> Xiao, Zhi-Cheng

<120> Peptides, Antibodies Thereto, and Their
Use in the Treatment of Central Nervous System Damage

<130> 0380-P03063US1

<140> US 10/537,648

<141> 2005-06-06

<150> PCT/GB2003/005323

<151> 2003-12-05

<150> US 60/431,620

<151> 2002-12-06

<160> 35

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> From a phage library that displays random 7-mers

<400> 1

Tyr Leu Thr Gln Pro Gln Ser
1 5

<210> 2

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> From a phage library that displays random 7-mers

<400> 2

Gly Ser Leu Pro His Ser Leu
1 5

<210> 3

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> From a phage library that displays random 7-mers

<400> 3

Thr Gln Leu Phe Pro Pro Gln
1 5

<210> 4

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> From a phage library that displays random 7-mers

<400> 4
His Ser Ile Pro Asp Asn Ile
1 5

<210> 5
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> From a phage library that displays random 7-mers

<400> 5
His His Met Pro His Asp Lys
1 5

<210> 6
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> From a phage library that displays random 7-mers

<400> 6
Tyr Thr Thr Pro Pro Ser Pro
1 5

<210> 7
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> From a phage library that displays random 7-mers

<400> 7
Gln Leu Pro Leu Met Pro Arg
1 5

<210> 8
<211> 508
<212> PRT
<213> Rattus norvegicus

<400> 8
Met Ile Phe Leu Thr Thr Leu Pro Leu Phe Trp Ile Met Ile Ser Ala
1 5 10 15
Ser Arg Gly Gly His Trp Gly Ala Trp Met Pro Ser Ser Ile Ser Ala
20 25 30
Phe Glu Gly Thr Cys Val Ser Ile Pro Cys Arg Phe Asp Phe Pro Asp
35 40 45
Glu Leu Arg Pro Ala Val Val His Gly Val Trp Tyr Phe Asn Ser Pro
50 55 60
Tyr Pro Lys Asn Tyr Pro Pro Val Val Phe Lys Ser Arg Thr Gln Val
65 70 75 80
Val His Glu Ser Phe Gln Gly Arg Ser Arg Leu Leu Gly Asp Leu Gly
85 90 95
Leu Arg Asn Cys Thr Leu Leu Leu Ser Thr Leu Ser Pro Glu Leu Gly
100 105 110
Gly Lys Tyr Tyr Phe Arg Gly Asp Leu Gly Gly Tyr Asn Gln Tyr Thr
115 120 125
Phe Ser Glu His Ser Val Leu Asp Ile Ile Asn Thr Pro Asn Ile Val
130 135 140
Val Pro Pro Glu Val Val Ala Gly Thr Glu Val Glu Val Ser Cys Met
145 150 155 160
Val Pro Asp Asn Cys Pro Glu Leu Arg Pro Glu Leu Ser Trp Leu Gly

				165						170					175				
His	Glu	Gly	Leu	Gly	Glu	Pro	Thr	Val	Leu	Gly	Arg	Leu	Arg	Glu	Asp				
			180						185					190					
Glu	Gly	Thr	Trp	Val	Gln	Val	Ser	Leu	Leu	His	Phe	Val	Pro	Thr	Arg				
		195					200					205							
Glu	Ala	Asn	Gly	His	Arg	Leu	Gly	Cys	Gln	Ala	Ala	Phe	Pro	Asn	Thr				
	210					215					220								
Thr	Leu	Gln	Phe	Glu	Gly	Tyr	Ala	Ser	Leu	Asp	Val	Lys	Tyr	Pro	Pro				
225					230					235					240				
Val	Ile	Val	Glu	Met	Asn	Ser	Ser	Val	Glu	Ala	Ile	Glu	Gly	Ser	His				
			245						250					255					
Val	Ser	Leu	Leu	Cys	Gly	Ala	Asp	Ser	Asn	Pro	Pro	Pro	Leu	Leu	Thr				
		260					265						270						
Trp	Met	Arg	Asp	Gly	Met	Val	Leu	Arg	Glu	Ala	Val	Ala	Glu	Ser	Leu				
	275						280					285							
Tyr	Leu	Asp	Leu	Glu	Glu	Val	Thr	Pro	Ala	Glu	Asp	Gly	Ile	Tyr	Ala				
	290					295					300								
Cys	Leu	Ala	Glu	Asn	Ala	Tyr	Gly	Gln	Asp	Asn	Arg	Thr	Val	Glu	Leu				
305					310					315					320				
Ser	Val	Met	Tyr	Ala	Pro	Trp	Lys	Pro	Thr	Val	Asn	Gly	Thr	Val	Val				
		325							330					335					
Ala	Val	Glu	Gly	Glu	Thr	Val	Ser	Ile	Leu	Cys	Ser	Thr	Gln	Ser	Asn				
	340							345					350						
Pro	Asp	Pro	Ile	Leu	Thr	Ile	Phe	Lys	Glu	Lys	Gln	Ile	Leu	Ala	Thr				
	355						360					365							
Val	Ile	Tyr	Glu	Ser	Gln	Leu	Gln	Leu	Glu	Leu	Pro	Ala	Val	Thr	Pro				
	370					375					380								
Glu	Asp	Asp	Gly	Glu	Tyr	Trp	Cys	Val	Ala	Glu	Asn	Gln	Tyr	Gly	Gln				
385					390					395					400				
Arg	Ala	Thr	Ala	Phe	Asn	Leu	Ser	Val	Glu	Phe	Ala	Pro	Ile	Ile	Leu				
		405							410					415					
Leu	Glu	Ser	His	Cys	Ala	Ala	Ala	Arg	Asp	Thr	Val	Gln	Cys	Leu	Cys				
	420							425					430						
Val	Val	Lys	Ser	Asn	Pro	Glu	Pro	Ser	Val	Ala	Phe	Glu	Leu	Pro	Ser				
	435						440					445							
Arg	Asn	Val	Thr	Val	Asn	Glu	Thr	Glu	Arg	Glu	Phe	Val	Tyr	Ser	Glu				
	450					455					460								
Arg	Ser	Gly	Leu	Leu	Leu	Thr	Ser	Ile	Leu	Thr	Leu	Arg	Gly	Gln	Ala				
465					470					475					480				
Gln	Ala	Pro	Pro	Arg	Val	Ile	Cys	Thr	Ser	Arg	Asn	Leu	Tyr	Gly	Thr				
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Gln	Ser	Leu	Glu	Leu	Pro	Phe	Gln	Gly	Ala	His	Arg								
		500						505											

<210> 9
 <211> 205
 <212> PRT
 <213> Homo sapiens

<400> 9

Cys	Pro	Cys	Ala	Ser	Ser	Ala	Gln	Val	Leu	Gln	Glu	Leu	Leu	Ser	Arg				
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Ile	Glu	Met	Leu	Glu	Arg	Glu	Val	Ser	Val	Leu	Arg	Asp	Gln	Cys	Asn				
		20						25					30						
Ala	Asn	Cys	Cys	Gln	Glu	Ser	Ala	Ala	Thr	Gly	Gln	Leu	Asp	Tyr	Ile				
	35						40					45							
Pro	His	Cys	Ser	Gly	His	Gly	Asn	Phe	Ser	Phe	Glu	Ser	Cys	Gly	Cys				
	50					55					60								
Ile	Cys	Asn	Glu	Gly	Trp	Phe	Gly	Lys	Asn	Cys	Ser	Glu	Pro	Tyr	Cys				
65					70					75					80				
Pro	Leu	Gly	Cys	Ser	Ser	Arg	Gly	Val	Cys	Val	Asp	Gly	Gln	Cys	Ile				
		85							90					95					
Cys	Asp	Ser	Glu	Tyr	Ser	Gly	Asp	Asp	Cys	Ser	Glu	Leu	Arg	Cys	Pro				
	100							105					110						
Thr	Asp	Cys	Ser	Ser	Arg	Gly	Leu	Cys	Val	Asp	Gly	Glu	Cys	Val	Cys				
	115						120					125							
Glu	Glu	Pro	Tyr	Thr	Gly	Glu	Asp	Cys	Arg	Glu	Leu	Arg	Cys	Pro	Gly				
	130					135					140								
Asp	Cys	Ser	Gly	Lys	Gly	Arg	Cys	Ala	Asn	Gly	Thr	Cys	Leu	Cys	Glu				
145					150					155					160				

Glu	Gly	Tyr	Val	Gly	Glu	Asp	Cys	Gly	Gln	Arg	Gln	Cys	Leu	Asn	Ala
				165					170					175	
Cys	Ser	Gly	Arg	Gly	Gln	Cys	Glu	Glu	Gly	Leu	Cys	Val	Cys	Glu	Glu
			180					185					190		
Gly	Tyr	Gln	Gly	Pro	Asp	Cys	Ser	Ala	Val	Ala	Pro	Pro			
	195						200					205			

<210> 10
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 <212> PRT
 <213> Homo sapiens

<400> 10															
Met	Glu	Asp	Leu	Asp	Gln	Ser	Pro	Leu	Val	Ser	Ser	Ser	Asp	Ser	Pro
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Pro	Arg	Pro	Gln	Pro	Ala	Phe	Lys	Tyr	Gln	Phe	Val	Arg	Glu	Pro	Glu
			20					25					30		
Asp	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Glu	Asp	Glu	Asp	
		35				40					45				
Leu	Glu	Glu	Leu	Glu	Val	Leu	Glu	Arg	Lys	Pro	Ala	Ala	Gly	Leu	Ser
	50				55						60				
Ala	Ala	Pro	Val	Pro	Thr	Ala	Pro	Ala	Ala	Gly	Ala	Pro	Leu	Met	Asp
65					70				75					80	
Phe	Gly	Asn	Asp	Phe	Val	Pro	Pro	Ala	Pro	Arg	Gly	Pro	Leu	Pro	Ala
			85					90					95		
Ala	Pro	Pro	Val	Ala	Pro	Glu	Arg	Gln	Pro	Ser	Trp	Asp	Pro	Ser	Pro
			100					105					110		
Val	Ser	Ser	Thr	Val	Pro	Ala	Pro	Ser	Pro	Leu	Ser	Ala	Ala	Ala	Val
		115					120					125			
Ser	Pro	Ser	Lys	Leu	Pro	Glu	Asp	Asp	Glu	Pro	Pro	Ala	Arg	Pro	Pro
	130					135						140			
Pro	Pro	Pro	Pro	Ala	Ser	Val	Ser	Pro	Gln	Ala	Glu	Pro	Val	Trp	Thr
145					150				155					160	
Pro	Pro	Ala	Pro	Ala	Pro	Ala	Ala	Pro	Pro	Ser	Thr	Pro	Ala	Ala	Pro
			165					170						175	
Lys	Arg	Arg	Gly	Ser	Ser	Gly	Ser	Val							
			180					185							

<210> 11
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 <212> PRT
 <213> Homo sapiens

<400> 11															
Arg	Ile	Tyr	Lys	Gly	Val	Ile	Gln	Ala	Ile	Gln	Lys	Ser	Asp	Glu	Gly
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His	Pro	Phe	Arg	Ala	Tyr	Leu	Glu	Ser	Glu	Val	Ala	Ile	Ser	Glu	Glu
			20					25					30		
Leu	Val	Gln	Lys	Tyr	Ser	Asn	Ser	Ala	Leu	Gly	His	Val	Asn	Cys	Thr
		35				40						45			
Ile	Lys	Glu	Leu	Arg	Arg	Leu	Phe	Leu	Val	Asp	Asp	Leu	Val	Asp	Ser
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Leu	Lys														
65															

<210> 12
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fusion protein

<220>
 <221> VARIANT
 <222> (509)...(511)
 <223> Polyalanine linker

<220>
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 <222> (717)...(719)
 <223> Polyalanine linker

<220>
 <221> VARIANT
 <222> (905)...(907)
 <223> Polyalanine linker

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 Ser Arg Gly Gly His Trp Gly Ala Trp Met Pro Ser Ser Ile Ser Ala
 20 25 30
 Phe Glu Gly Thr Cys Val Ser Ile Pro Cys Arg Phe Asp Phe Pro Asp
 35 40 45
 Glu Leu Arg Pro Ala Val Val His Gly Val Trp Tyr Phe Asn Ser Pro
 50 55 60
 Tyr Pro Lys Asn Tyr Pro Pro Val Val Phe Lys Ser Arg Thr Gln Val
 65 70 75 80
 Val His Glu Ser Phe Gln Gly Arg Ser Arg Leu Leu Gly Asp Leu Gly
 85 90 95
 Leu Arg Asn Cys Thr Leu Leu Leu Ser Thr Leu Ser Pro Glu Leu Gly
 100 105 110
 Gly Lys Tyr Tyr Phe Arg Gly Asp Leu Gly Gly Tyr Asn Gln Tyr Thr
 115 120 125
 Phe Ser Glu His Ser Val Leu Asp Ile Ile Asn Thr Pro Asn Ile Val
 130 135 140
 Val Pro Pro Glu Val Val Ala Gly Thr Glu Val Glu Val Ser Cys Met
 145 150 155 160
 Val Pro Asp Asn Cys Pro Glu Leu Arg Pro Glu Leu Ser Trp Leu Gly
 165 170 175
 His Glu Gly Leu Gly Glu Pro Thr Val Leu Gly Arg Leu Arg Glu Asp
 180 185 190
 Glu Gly Thr Trp Val Gln Val Ser Leu Leu His Phe Val Pro Thr Arg
 195 200 205
 Glu Ala Asn Gly His Arg Leu Gly Cys Gln Ala Ala Phe Pro Asn Thr
 210 215 220
 Thr Leu Gln Phe Glu Gly Tyr Ala Ser Leu Asp Val Lys Tyr Pro Pro
 225 230 235 240
 Val Ile Val Glu Met Asn Ser Ser Val Glu Ala Ile Glu Gly Ser His
 245 250 255
 Val Ser Leu Leu Cys Gly Ala Asp Ser Asn Pro Pro Pro Leu Leu Thr
 260 265 270
 Trp Met Arg Asp Gly Met Val Leu Arg Glu Ala Val Ala Glu Ser Leu
 275 280 285
 Tyr Leu Asp Leu Glu Glu Val Thr Pro Ala Glu Asp Gly Ile Tyr Ala
 290 295 300
 Cys Leu Ala Glu Asn Ala Tyr Gly Gln Asp Asn Arg Thr Val Glu Leu
 305 310 315 320
 Ser Val Met Tyr Ala Pro Trp Lys Pro Thr Val Asn Gly Thr Val Val
 325 330 335
 Ala Val Glu Gly Glu Thr Val Ser Ile Leu Cys Ser Thr Gln Ser Asn
 340 345 350
 Pro Asp Pro Ile Leu Thr Ile Phe Lys Glu Lys Gln Ile Leu Ala Thr
 355 360 365
 Val Ile Tyr Glu Ser Gln Leu Gln Leu Glu Leu Pro Ala Val Thr Pro
 370 375 380
 Glu Asp Asp Gly Glu Tyr Trp Cys Val Ala Glu Asn Gln Tyr Gly Gln
 385 390 395 400
 Arg Ala Thr Ala Phe Asn Leu Ser Val Glu Phe Ala Pro Ile Ile Leu
 405 410 415
 Leu Glu Ser His Cys Ala Ala Ala Arg Asp Thr Val Gln Cys Leu Cys
 420 425 430
 Val Val Lys Ser Asn Pro Glu Pro Ser Val Ala Phe Glu Leu Pro Ser
 435 440 445
 Arg Asn Val Thr Val Asn Glu Thr Glu Arg Glu Phe Val Tyr Ser Glu
 450 455 460
 Arg Ser Gly Leu Leu Leu Thr Ser Ile Leu Thr Leu Arg Gly Gln Ala
 465 470 475 480

Gln	Ala	Pro	Pro	Arg	Val	Ile	Cys	Thr	Ser	Arg	Asn	Leu	Tyr	Gly	Thr
				485					490					495	
Gln	Ser	Leu	Glu	Leu	Pro	Phe	Gln	Gly	Ala	His	Arg	Ala	Ala	Ala	Cys
			500					505					510		
Pro	Cys	Ala	Ser	Ser	Ala	Gln	Val	Leu	Gln	Glu	Leu	Leu	Ser	Arg	Ile
			515				520					525			
Glu	Met	Leu	Glu	Arg	Glu	Val	Ser	Val	Leu	Arg	Asp	Gln	Cys	Asn	Ala
	530					535					540				
Asn	Cys	Cys	Gln	Glu	Ser	Ala	Ala	Thr	Gly	Gln	Leu	Asp	Tyr	Ile	Pro
545					550					555					560
His	Cys	Ser	Gly	His	Gly	Asn	Phe	Ser	Phe	Glu	Ser	Cys	Gly	Cys	Ile
			565						570					575	
Cys	Asn	Glu	Gly	Trp	Phe	Gly	Lys	Asn	Cys	Ser	Glu	Pro	Tyr	Cys	Pro
			580					585					590		
Leu	Gly	Cys	Ser	Ser	Arg	Gly	Val	Cys	Val	Asp	Gly	Gln	Cys	Ile	Cys
			595				600					605			
Asp	Ser	Glu	Tyr	Ser	Gly	Asp	Asp	Cys	Ser	Glu	Leu	Arg	Cys	Pro	Thr
	610					615					620				
Asp	Cys	Ser	Ser	Arg	Gly	Leu	Cys	Val	Asp	Gly	Glu	Cys	Val	Cys	Glu
625					630					635					640
Glu	Pro	Tyr	Thr	Gly	Glu	Asp	Cys	Arg	Glu	Leu	Arg	Cys	Pro	Gly	Asp
				645					650					655	
Cys	Ser	Gly	Lys	Gly	Arg	Cys	Ala	Asn	Gly	Thr	Cys	Leu	Cys	Glu	Glu
			660					665					670		
Gly	Tyr	Val	Gly	Glu	Asp	Cys	Gly	Gln	Arg	Gln	Cys	Leu	Asn	Ala	Cys
			675				680					685			
Ser	Gly	Arg	Gly	Gln	Cys	Glu	Glu	Gly	Leu	Cys	Val	Cys	Glu	Glu	Gly
	690					695					700				
Tyr	Gln	Gly	Pro	Asp	Cys	Ser	Ala	Val	Ala	Pro	Pro	Ala	Ala	Ala	Met
705					710					715					720
Glu	Asp	Leu	Asp	Gln	Ser	Pro	Leu	Val	Ser	Ser	Ser	Asp	Ser	Pro	Pro
				725					730					735	
Arg	Pro	Gln	Pro	Ala	Phe	Lys	Tyr	Gln	Phe	Val	Arg	Glu	Pro	Glu	Asp
			740					745					750		
Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Glu	Asp	Glu	Asp	Leu
			755				760					765			
Glu	Glu	Leu	Glu	Val	Leu	Glu	Arg	Lys	Pro	Ala	Ala	Gly	Leu	Ser	Ala
			770			775					780				
Ala	Pro	Val	Pro	Thr	Ala	Pro	Ala	Ala	Gly	Ala	Pro	Leu	Met	Asp	Phe
785					790					795					800
Gly	Asn	Asp	Phe	Val	Pro	Pro	Ala	Pro	Arg	Gly	Pro	Leu	Pro	Ala	Ala
				805					810					815	
Pro	Pro	Val	Ala	Pro	Glu	Arg	Gln	Pro	Ser	Trp	Asp	Pro	Ser	Pro	Val
			820					825					830		
Ser	Ser	Thr	Val	Pro	Ala	Pro	Ser	Pro	Leu	Ser	Ala	Ala	Ala	Val	Ser
			835				840					845			
Pro	Ser	Lys	Leu	Pro	Glu	Asp	Asp	Glu	Pro	Pro	Ala	Arg	Pro	Pro	Pro
						855					860				
Pro	Pro	Pro	Ala	Ser	Val	Ser	Pro	Gln	Ala	Glu	Pro	Val	Trp	Thr	Pro
865					870					875					880
Pro	Ala	Pro	Ala	Pro	Ala	Ala	Pro	Pro	Ser	Thr	Pro	Ala	Ala	Pro	Lys
				885					890					895	
Arg	Arg	Gly	Ser	Ser	Gly	Ser	Val	Ala	Ala	Ala	Arg	Ile	Tyr	Lys	Gly
			900					905					910		
Val	Ile	Gln	Ala	Ile	Gln	Lys	Ser	Asp	Glu	Gly	His	Pro	Phe	Arg	Ala
			915				920					925			
Tyr	Leu	Glu	Ser	Glu	Val	Ala	Ile	Ser	Glu	Glu	Leu	Val	Gln	Lys	Tyr
	930					935					940				
Ser	Asn	Ser	Ala	Leu	Gly	His	Val	Asn	Cys	Thr	Ile	Lys	Glu	Leu	Arg
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Arg	Leu	Phe	Leu	Val	Asp	Asp	Leu	Val	Asp	Ser	Leu	Lys			
				965					970						

<210> 13

<211> 1524

<212> DNA

<213> Rattus norvegicus

<400> 13

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ccctgcccgtt	tcgacttccc	ggatgagctc	agaccggctg	tggtacatgg	cgtctgggat	180
ttcaacagtc	ccatcccaca	gaactaccgc	ccagtggtct	tcaagtcccg	cacacaagtg	240
gtccacgaga	gcttccaggg	ccgtagccgc	ctgttgggag	acctgggcct	acgaaactgc	300
accctgcttc	tcagcacgct	gagccctgag	ctggggaggga	aatactatct	ccgaggtgac	360
ctggggcggtc	acaaccagta	caccttctcg	gagcacagcg	tcctggacat	catcaacacc	420
cccaacatcg	tggtgcccc	agaagtgggtg	gcaggaacgg	aagtagaggt	cagctgcatg	480
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ctgtctacact	tcgtgcctac	tagagaggcc	aacggccacc	gtctgggctg	tcaggctgcc	660
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gtgattgtgg	agatgaattc	ctctgtggag	gccattgagg	gctcccacgt	cagcctgtct	780
tgtggggctg	acagcaaccc	gccaccgctg	ctgacttgga	tcggggatgg	gatggtgttg	840
agggaggcag	ttgctgagag	cctgtacctg	gatctggagg	aggtgacccc	agcagaggac	900
ggcatctatg	cttgccctggc	agagaatgcc	tatggccagg	acaaccgcac	ggtggagctg	960
agcgtcatgt	atgcaccttg	gaagcccaca	gtgaatggga	cggtgggtggc	ggtagagggg	1020
gagacagtct	ccatcctgtg	ttccacacag	agcaaccgag	acctattctt	caccatcttc	1080
aaggagaagc	agatcctggc	cacggctcatc	tatgagagtc	agctgcagct	ggaactccct	1140
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tccgtggcct	ttgagctgcc	ttcccgcac	gtgactgtga	acgagacaga	gagggagttt	1380
gtgtactcag	atcgacggcg	cctcctgtct	accagcatcc	tcacgctccg	gggtcaggcc	1440
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<210> 14
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 <212> DNA
 <213> Homo sapiens

<400> 14						
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gccacaggac	aactggacta	tatccctcac	tcagctggcc	acggcaactt	tagctttgag	180
tccctgtggct	gcatctgcaa	cgaaggctgg	tttggcaaga	attgctcgga	gccctactgc	240
ccgctggggtt	gctccagccg	gggggtgtgt	gtggatggcc	agtgcactct	tgacagcgaa	300
tacagcgggg	atgactgttc	cgaactccgg	tgcccaacag	actgcagctc	ccgggggctc	360
tgctgtggacg	gggagtgtgt	ctgtgaagag	ccctacactg	gcgaggactg	cagggaactg	420
aggtgcctcg	gggactgttc	ggggaagggt	agatgtgcca	acggtaacctg	tttatgagag	480
gagggctacg	ttggtgagga	ctgcggccag	cggcagtgtc	tgaatgcctg	cagtgggcga	540
ggacaatgtg	aggaggggct	ctgcgtctgt	gaagagggtc	accagggccc	tgactgtctc	600
gcagttgccc	ctcca					615

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 <212> DNA
 <213> Homo sapiens

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gaagaggagg	acgaggacga	agacctggag	gagctggagg	tgctggagag	gaagcccggc	180
gccgggctgt	ccgcggcccc	agtccccacc	gccccctgcc	ccggcgcgccc	cctgatggac	240
ttcggaatg	acttcgtgcc	gccggcgccc	cggggacccc	tgccggcgcc	ttcccccgctc	300
gccccggagc	ggcagccgtc	ttgggacccg	agccccgtgt	cgtcgaccgt	gccccgcgcca	360
ttccccgctgt	ctgctgccgc	agtctcgccc	tccaagctcc	ctgaggacga	cgagcctccg	420
gccccgcctc	ccccctctcc	cccggccagc	gtgagccccc	aggcagagcc	cgtgtggacc	480
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<210> 16
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 <212> DNA
 <213> Homo sapiens

<400> 16						
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gctcttggtc	atgtgaactg	cacgataaag	gaactcaggc	gcctcttctt	agttgatgat	180
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<210> 17
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 <220>
 <223> PCR primer MAG1

 <400> 17
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 <210> 18
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR primer MAG2

 <400> 18
 tccccgcggc tcggtgtgct ccctggaa 28

 <210> 19
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR primer TNR1

 <400> 19
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 <210> 20
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 <220>
 <223> PCR primer TNR2

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 <210> 21
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 <220>
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 <210> 22
 <211> 31
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 <400> 22
 aaactgcagc cactgagccc gaggagcccc t 31

 <210> 23
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 <212> DNA
 <213> Artificial Sequence

<220>
<223> PCR primer Nogo66-1

<400> 23
aaactgcagc aaggatatac aaggggtgt

28

<210> 24
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer Nogo66-2

<400> 24
gctctagatc acttcagaga atcaacta

28

<210> 25
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<212> DNA
<213> Artificial Sequence

<220>
<223> Construct resulting from sequentially connected
PCR products

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gagttgggtc agaagtacag taattctgct cttgggtcatg tgaactgcac gataaaggaa 2880
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<210> 26
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<213> M13 coliphage

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<400> 26
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<210> 27
<211> 33
<212> DNA
<213> M13 coliphage

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<400> 27
ggtggagggt cggccgaaac tgttgaaagt tgt 33

```

```

<210> 28
<211> 21
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Exemplary 7-mer peptide-encoding sequence

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<400> 28
tatctgacgc agcctcagtc g 21

```

```

<210> 29
<211> 21
<212> DNA
<213> Artificial Sequence

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<220>
<223> Exemplary 7-mer peptide-encoding sequence

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<400> 29
ggttctctgc ctcattcgct g 21

```

```

<210> 30
<211> 21
<212> DNA
<213> Artificial Sequence

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<220>
<223> Exemplary 7-mer peptide-encoding sequence

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<400> 30
acgcagctgt ttcctcctta g 21

```

```

<210> 31
<211> 21
<212> DNA
<213> Artificial Sequence

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<220>
<223> Exemplary 7-mer peptide-encoding sequence

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<400> 31
cattctattc ctgataatat t 21

```

```

<210> 32
<211> 21
<212> DNA
<213> Artificial Sequence

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<220>
<223> Exemplary 7-mer peptide-encoding sequence

<400> 32
catcatatgc ctcatgataa g 21

<210> 33
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
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tatacgacgc ctccgagtcc t 21

<210> 34
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<223> Exemplary 7-mer peptide-encoding sequence

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cagcttccgc ttatgcctcg t 21

<210> 35
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary 7-mer peptide-encoding sequence

<400> 35
acgcagctgt ttctctctca g 21